

Figure 1A

1 CACCCATATCC TACACTACTA GGAACCTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
 121 GCAGCCAAAC GCCTCCCTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
 181 AGGCCTGAAG GAACAGGCCG GGGAGGAGC CCTCCCTCTC TCCCTGTCC CTCCATCCAC 240  
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
 1 M A R A H W G C C P W L 12  
 301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
 13 V L L C A C A W G H T K P L D L G G Q D 32  
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
 33 V R N C S T N P P Y L P V T V V N T T M 52  
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAACATG ACGAGAGGCG TGCGTGGATT 540  
 73 G T D A H M N E Y I G Q H D E R R A W I 92  
 541 ACAGGCTTTA CAGGGTCTGC AGGAACGTGCA GTGGTGAUTA TGAAGAAAGC AGCTGTCTGG 600  
 93 T G F T G S A G T A V V T M K K A A V W 112  
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
 113 T D S R Y W T Q A E R Q M D C N W E L H 132  
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720  
 133 K E V G T T P I V T W L L T E I P A G G 152  
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGC 780  
 153 R V G F D P F L L S I D T W E S Y D L A 172  
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840  
 173 L Q G S N R Q L V S I T T N L V D L V W 192  
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900  
 193 G S E R P P V P N Q P I Y A L Q E A F T 212  
 901 GGGAGCACTT GGCAGGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 1B

961 GTCCCGACTG CCGTCCTTCT GTCGGCCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
 233 V P T A V L L S A L E E T A W L F N L R 252  
  
 1021 GCCAGTGACA TCCCCTATAA CCCCTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080  
 253 A S D I P Y N P F F Y S Y T L L T D S S 272  
  
 1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
 273 I R L F A N K S R F S S E T L S Y L N S 292  
  
 1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
 293 S C T G P M C V Q I E D Y S Q V R D S I 312  
  
 1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332  
  
 1261 ATCTATGAAA TGATACCAAG GGAGAAAATC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
 333 I Y E M I P R E K L V T D T Y S P V M M 352  
  
 1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
 353 T K A V K N S K E Q A L L K A S H V R D 372  
  
 1381 GCTGTGGCTG TGATCCGTA CTGGTCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440  
 373 A V A V I R Y L V W L E K N V P K G T V 392  
  
 1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
 393 D E F S G A E I V D K F R G E E Q F S S 412  
  
 1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAAATG CTGCCCTGGC CCACTACAGC 1560  
 413 G P S F E T I S A S G L N A A L A H Y S 432  
  
 1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
 433 P T K E L N R K L S S D E M Y L L D S G 452  
  
 1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
 453 G Q Y W D G T T D I T R T V H W G T P S 472  
  
 1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
 473 A F Q K E A Y T R V L I G N I D L S R L 492  
  
 1741 ATCTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800  
 493 I F P A A T S G R M V E A F A R R A L W 512  
  
 1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCGAGTG GCTCAACAGCACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTGCAATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCATAAT CCCAGGGCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCATA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

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**Figure 1D**

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

Figure 2A

1 CACCCATATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
 181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTGTCC CTCCATCCAC 240  
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
 1 M A R A H W G C C P W L 12  
 301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
 13 V L L C A C A W G H T K P L D L G G Q D 32  
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
 33 V R N C S T N P P Y L P V T V V N T T M 52  
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAAC TCTCAGCCTA CATCATCCCA 480  
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAACATG ACGAGAGCCG TGCGTGGATT 540  
 73 G T D A H M N E Y I G Q H D E R R A W I 92  
 541 ACAGGTTTA CAGGGTCTGC AGGAAC TGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600  
 93 T G F T G S A G T A V V T M K K A A V W 112  
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
 113 T D S R Y W T Q A E R Q M D C N W E L H 132  
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720  
 133 K E V G T T P I V T W L L T E I P A G G 152  
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
 153 R V G F D P F L L S I D T W E S Y D L A 172  
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840  
 173 L Q G S N R Q L V S I T T N L V D L V W 192  
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900  
 193 G S E R P P V P N Q P I Y A L Q E A F T 212  
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAG 960  
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

D0053 NP

Figure 2B

961 GTCCCGACTG CCGTCCTTCT GTCGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTCTTC TATTCTACCA CGCTGCTCAC AGACTCTTCT 1080  
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAAATC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGTA CTTGGTCTGG CTGGAGAAGA ACGTCCCCAA AGGCACAGTG 1440  
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560  
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCCGAG AGCCTTGTTG 1800  
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTG 1860  
513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCTCA CCCTGCCTG AACATAACCC AAGAGCCCC GCTGGCCCAT TGCCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGACTAA 2940

D0053 NP

**Figure 2D**

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCTCAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

Figure 3A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAC CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

**Figure 3B**

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTG ATGTCTTG GT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 4A

1 CTGTGCATGG CATCATCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCTGGTCT GCTGGCCCC TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 4B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTG GT GGGCCAGCTC 960  
299 F F A F T N S S L N P V I Y V F V G Q L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 5A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCAA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCATT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 5B

901 TTCTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

D0053 NP

Figure 6A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTT CTGTCTGTC GTGAGGACTC CGTGCACC 60  
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTAACGGG 120  
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240  
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360  
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCAATC 720  
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 6B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC T TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTAA 1620

1621 TCTATTCAAG TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT ACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

**Figure 6C**

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAACGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 6D**

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

Figure 7A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTT 120  
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
 1 M D N V L P V D S D 10  
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
 11 L S P N I S T N T S E P N Q F V Q P A W 30  
 301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
 31 Q I V L W A A A Y T V I V V T S V V G N 50  
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420  
 51 V V V M W I I L A H K R M R T V T N Y F 70  
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
 71 L V N L A F A E A S M A A F N T V V N F 90  
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540  
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
 111 F P I A A V F A S I Y S M T A V A F D R 130  
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCA CCACAGCCAC CAAAGTGGTC 660  
 131 Y M A I I H P L Q P R L S A T A T K V V 150  
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720  
 151 I C V I W V L A L L L A F P Q G Y Y S T 170  
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
 171 T E T M P S R V V C M I E W P E H P N K 190  
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840  
 191 I Y E K V Y H I C V T V L I Y F L P L L 210  
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
 211 V I G Y A Y T V V G I T L W A S E I P G 230  
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
 231 D S S D R Y H E Q V S A K R K V V K M M 250

D0053 NP

Figure 7B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAAGCCGCC TGGAGACAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTACACGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCTTTGG CAGGTGCAGC CCCCAC TGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTGGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTG AGGATG 1766

D0053 NP

Figure 8A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTT 120  
121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
1 M D N V L P V D S D 10  
241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
11 L S P N I S T N T S E P N Q F V Q P A W 30  
301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
31 Q I V L W A A A Y T V I V V T S V V G N 50  
361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAACATGA GGACAGTGAC GAACTATTTT 420  
51 V V V M W I I L A H K R M R T V T N Y F 70  
421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
71 L V N L A F A E A S M A A F N T V V N F 90  
481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540  
91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
111 F P I A A V F A S I Y S M T A V A F D R 130  
601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660  
131 Y M A I I H P L Q P R L S A T A T K V V 150  
661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTC CCCAGGGCTA CTACTCAACC 720  
151 I C V I W V L A L L L A F P Q G Y Y S T 170  
721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
171 T E T M P S R V V C M I E W P E H P N K 190  
781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840  
191 I Y E K V Y H I C V T V L I Y F L P L L 210  
841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
211 V I G Y A Y T V V G I T L W A S E I P G 230  
901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
231 D S S D R Y H E Q V S A K R K V V K M M 250

D0053 NP

Figure 8B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTACACGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCTTTGG CAGGTGCAGC CCCCAC TGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTGGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTTC AGGATG 1766

**Figure 9A**

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTATA TTCTGAGCGC 60  
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120  
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGG GGGTTGTGTA 180  
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
 1 M D N V L P V D S D 10  
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
 11 L S P N I S T N T S E P N Q F V Q P A W 30  
 301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
 31 Q I V L W A A A Y T V I V V T S V V G N 50  
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAACATGA GGACAGTGAC GAACTATTTT 420  
 51 V V V M W I I L A H K R M R T V T N Y F 70  
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
 71 L V N L A F A E A S M A A F N T V V N F 90  
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540  
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
 111 F P I A A V F A S I Y S M T A V A F D R 130  
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAAG CCACAGCCAC CAAAGTGGTC 660  
 131 Y M A I I H P L Q P R L S A T A T K V V 150  
 661 ATCTGTGTCA TATGGGTCCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720  
 151 I C V I W V L A L L L A F P Q G Y Y S T 170  
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
 171 T E T M P S R V V C M I E W P E H P N K 190  
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840  
 191 I Y E K V Y H I C V T V L I Y F L P L L 210  
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
 211 V I G Y A Y T V V G I T L W A S E I P G 230  
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
 231 D S S D R Y H E Q V S A K R K V V K M M 250

D0053 NP

Figure 9B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTACCGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCTTTGG CAGGTGCAGC CCCCAC TGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTTC AGGATG 1766

D0053 NP

Figure 10A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
61 CAGTTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120  
121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
1 M D N V L P V D S D 10  
241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCTGCA ACCAGCCTGG 300  
11 L S P N I S T N T S E P N Q F V Q P A W 30  
301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
31 Q I V L W A A A Y T V I V V T S V V G N 50  
361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAACATGA GGACAGTGAC GAACTATTTT 420  
51 V V V M W I I L A H K R M R T V T N Y F 70  
421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
71 L V N L A F A E A S M A A F N T V V N F 90  
481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540  
91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
111 F P I A A V F A S I Y S M T A V A F D R 130  
601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAAG CCACAGCCAC CAAAGTGGTC 660  
131 Y M A I I H P L Q P R L S A T A T K V V 150  
661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720  
151 I C V I W V L A L L L A F P Q G Y Y S T 170  
721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
171 T E T M P S R V V C M I E W P E H P N K 190  
781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840  
191 I Y E K V Y H I C V T V L I Y F L P L L 210  
841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
211 V I G Y A Y T V V G I T L W A S E I P G 230  
901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
231 D S S D R Y H E Q V S A K R K V V K M M 250

D0053 NP

Figure 10B

961 ATTGTGCGTGG TGTGCACCTT CGCCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCCTG GACCTGACCT CCAAATGCTC TTACCGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCTTTGG CAGGTGCAGC CCCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

Figure 11A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTGTTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F V E P I L 60  
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCAACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
 141 V L G D A L V D F S L K L Y H A F S A M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTACGCC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC ACAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

D0053 NP

Figure 11B

961 ACAACATTTG ATCCCAAGAA AACAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

D0053 NP

Figure 12A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGAGT CCGCTGACGT CGCCGCCAG 60  
61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
1 M A S R L T L L T L L L L L A G D R A 20  
121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
21 S S N P N A T S S S S Q D P E S L Q D R 40  
181 GGCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTGTTGA ACCCATCCTG 240  
41 G E G K V A T T V I S K M L F V E P I L 60  
241 GAGGTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
61 E V S S L P T T N S T T N S A T K I T A 80  
301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
81 N T T D E P T T Q P T T E P T T Q P T I 100  
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
421 TCCTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
121 S F C P G P V T L C S D L E S H S T E A 140  
481 GTGTTGGGGG ATGTTGGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
141 V L G D A L V D F S L K L Y H A F S A M 160  
541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
161 K K V E T N M A F S P F S I A S L L T Q 180  
601 GTCCTGCTCG GGGCTGGCA GAACACAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
181 V L L G A G Q N T K T N L E S I L S Y P 200  
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGCTTCA CGACCAAAGG TGTACCTCA 720  
201 K D F T C V H Q A L K G F T T K G V T S 220  
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
221 V S Q I F H S P D L A I R D T F V N A S 240  
781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
241 R T L Y S S S P R V L S N N S D A N L E 260  
841 CTCATCAACA CCTGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
261 L I N T W V A K N T N N K I S R L L D S 280  
901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960  
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 12B

961 ACAACATTTG ATCCCAAGAA AACCAAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAA**T**GGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAG**T**CA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGA**A**CTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GCCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 13A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTGCTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F A E P I L 60  
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
 141 V L G D A L V D F S L K L Y H A F S A M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCTGCTCG GGGCTGGCA GAACACAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC ACAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

D0053 NP

Figure 13B

961 ACAACATTTG ATCCCAAGAA AACCGAGAATG GAACCCTTTC ACTTCAAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGA ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGGGGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AACACCTGACA GACCAT 1826

Figure 14A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F V E P I L 60  
 241 GAGGTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCCT CTCAGGAATG 540  
 141 V L G D A L V D F S L K L Y H A F S G M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

D0053 NP

Figure 14B

961 ACAACATTTG ATCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGA ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACCC CAGATCTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGGCGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 15A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F V E P I L 60  
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
 141 V L G D A L V D F S L K L Y H A F S A M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC ACAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 15B

961 ACAACATTTG ATCCCAGAAGAA AACCAAGATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACATTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGA ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAAATA AAACCTGACA GACCAT 1826

Figure 16

1 TCCTCCACCT GCTGGCCCC GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCCTGCG CCCCCGATTC AGTCCCGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCAC ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCGA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAA TTTCTCATTT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 17

1 TCCTCCACCT GCTGGCCCT GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCAC ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCGA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAA TTTCTCATTT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C E K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

**Figure 18**

1 TCCTCCACCT GCTGGCCCT GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG ACCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTCTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCCA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T Q E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAA TTTCTCATTT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

**Figure 19**

BRB1\_MOUSE MASQ . A S L K L Q P S N O S Q Q A P P N I T S C E G A P E A W D L L C R V L P G F V I T C F F G L L G N L L V L S  
 BRB1\_RAT MASE . V L L E L Q P S N R S L Q A P A N I T S C E S A L E D W D L L Y R V L P G F V I T I C F F G L L G N L L V L S  
 BRB1\_HUMAN MASSW P P L E L Q S S N Q S Q L F P O N A T A C D N A P E A W D L L H R V L P T F I S I C F F G L L G N L F V I L  
 BRB1\_RABIT MASQ . C P L E L Q P S N Q S Q L A P P N A T S C S G A P D A W D L L H R I L P T F I I A I F T L G L L G N S F V L S

BRB1\_MOUSE F F L L P W R R R W W . . . Q Q R R Q R L T I A E I Y L A N L A A S D L V F V L G L P F W A E N V G N R F N W P F G S D L  
 BRB1\_RAT F F L L P W R Q W W Q Q R Q R Q R L T I A E I Y L A N L A A S D L V F V L G L P F W A E N V G N R F N W P F G T D L  
 BRB1\_HUMAN V F L L P . . . . . . . R R Q L I N V A E I Y L A N L A A S D L V F V L G L P F W A E N V W N Q F N W P F G A I L  
 BRB1\_RABIT V F L L A . . . . . . . R R R L S V A E I Y L A N L A A S D L V F V L G L P F W A E N V R N Q F D W P F G A A L

BRB1\_MOUSE C R V V S G V I K A N L F I S I F L V V A I S Q D R Y R I L V Y P M T S W G I R R R R Q A Q V T C L L I W V A G G L L S  
 BRB1\_RAT C R V V S G V I K A N L F I S I F L V V A I S Q D R Y R I L V Y P M T S W G Y R R R R Q A Q V T C L L I W V A G G L L S  
 BRB1\_HUMAN C R V V N G V I K A N L F I S I F L V V A I S Q D R Y R I L V Y P M T S W G R I Q R R R Q A R V T C V I L I W V V G G L L S  
 BRB1\_RABIT C R V V N G V I K A N L F I S I F L V V A I S Q D R Y S V L V H P M A S R R G R R R R Q A Q V T C L I W V A G G L L S

BRB1\_MOUSE T P T F L L R S V K V V P D L N I S A C I L L F P H E A W H F V R M V E L N V L G F L L P L A A I L F N I H I L A S L  
 BRB1\_RAT I P T F L L R S V K V V P D L N I S A C I L L F P H E A W H F A R M V E L N V L G F L L P V T A I I F F N Y H I L A S L  
 BRB1\_HUMAN I P T F L L R S I Q A V P D L N I S A C I L L F P H E A W H F A R V E L N I L G F L L P L A A I V F F N Y H I L A S L  
 BRB1\_RABIT T P T F V L R S V R A V P I L N I S A C I L L F P H E A W H F L R M V E L N I L G F L L P L A A I L F F N C H I L A S L

\*

BRB1\_MOUSE R G Q K E A S R T R C G G P K D S K T M C L I L T L V A S F L V C W A P Y H F F A F L D F L V Q V R V I Q D C F W K E L  
 BRB1\_RAT R G Q K E A S R T R C G G P K G S K T T C L I L T L V A S F L V C W C P Y H F F A F L D F L V Q V R V I Q D C S W K E I  
 BRB1\_HUMAN R T R E E V S R T R V R G P K D S K T T A L I L T L V V A F L V C W A P Y H F F A F L E F L F Q V Q A V R G C F W E D F  
 BRB1\_RABIT R R R G E R V P R C G G P R D S K T A L I L T L V A S F L V C W A P Y H F F A F L E C L W Q V H A I G G C F W E F

\*

BRB1\_MOUSE T D L G L Q L A N F F A F V N S C L N P I I Y V F A G R L F K T R V L G T L ~~~~~~  
 BRB1\_RAT T D L G L Q L A N F F A F V N S C L N P I I Y V F A G R L L K T R V L G T L ~~~~~~  
 BRB1\_HUMAN I D L G L Q L A N F F A F T N S S L N P V I Y V F V G R L F R T K V W E L Y K Q C T P K S L A P I S S S H R K E I F Q L  
 BRB1\_RABIT T D L G L Q L S N F S A F V N S C L N P I I Y V F V G R L F R T K V W E L C Q Q C S P R S L A P I S S S R R K E M L W G

BRB1\_MOUSE ~~~~  
 BRB1\_RAT ~~~~  
 BRB1\_HUMAN F W R N  
 BRB1\_RABIT F W R N

**Figure 20**

|             |   |
|-------------|---|
| BRB2_MOUSE  | ~~~~~MPCSWKLLGFLSVHE.PMPTAASFGLEMFNVTQVLGSALNGTISKDN.CPDTEW   |
| BRB2_RAT    | MDTRSSLCP.KTQAVVAVFW.GPGCHLSTCIEMFNITQALGSAHNGTFSEVN.CPDTEW   |
| BRB2_RABBIT | ~~~~~MLNITSQVLAPALNGSVSQSSGCPNTIEW  |
| BRB2_CAVPO  | ~~~~~MFNITSQV..SALNATLAQGNSCLDAEW   |
| BRB2_HUMAN  | ~~~~~MFSPWKISMFISVREDSVPTTASFSADMNLNVTLQ..GPTLNGTFAQ.SKCPQVEW   |
| BRB2_MOUSE  | WSWLNAIQAPFLWVLFLAALENFVLSVFFLHKNSCTVAEIYLGNLAAADLILACGLPF  |
| BRB2_RAT    | WSWLNAIQAPFLWVLFLAALENIFVLSVFCLHKNSCTVAEIYLGNLAAADLILACGLPF   |
| BRB2_RABBIT | SGWLNVIQAPFLWVLFLVLATLENFVLSVFCLHKSSCTVAEIYLGNLAAADLILACGLPF  |
| BRB2_CAVPO  | WSWLNTIQAPFLWVLFLVLALENIFVLSVFFLHKSSCTVAEIYLGNLAAADLILACGLPF  |
| BRB2_HUMAN  | LGWLNТИQPPFLWVLFLVLATLENIFVLSVFCLHKSSCTVAEIYLGNLAAADLILACGLPF   |
| BRB2_MOUSE  | WAITIANNFDW <del>I</del> FGEVLCRVVNTMIYMNLSSICFLMLVSIDRYLALVKTMSMGRMRGV   |
| BRB2_RAT    | WAITIANNFDWLFGEVLCRVVNTMIYMNLSSICFLMLVSIDRYLALVKTMSMGRMRGV  |
| BRB2_RABBIT | WAITIANHFDWLFGEALCRVVNTMIYMNLSSICFLMLVSIDRYLALVKTMSMGRMRGV  |
| BRB2_CAVPO  | WAITIANNFDWLFGEVLCR <del>V</del> NNTMIQMNLSSICFLMLVSIDRYLALVKTMSMGRMRGV   |
| BRB2_HUMAN  | WAITISNNFDWLFGETLCRVVNA <del>T</del> ISMNLSSICFLMLVSIDRYLALVKTMSMGRMRGV   |
| BRB2_MOUSE  | WAKLYSLVIWGCTLLLSSPMLVFRTM <del>E</del> YSEEGHNVTACVIVYPSRSWEVFTNVLLNLVG  |
| BRB2_RAT    | WAKLYSLVIWSCTLLLSSPMLVFRTMKD <del>Y</del> RSEEGHNVTACVIVYPSRSWEVFTNM <del>M</del> NNLVG   |
| BRB2_RABBIT | WAKLYSLVIWGCTLLLSSPMLVFRTMKD <del>Y</del> RDEGYNVTACIIDYPSRSWEVFTNVLLNLVG   |
| BRB2_CAVPO  | WAKLYSLVIWGCA <del>L</del> LLLSSPMLVFRTMKD <del>Y</del> RDEGHNVTACI <del>I</del> YPSL <del>I</del> WQVFTNVLLNLVG                              |
| BRB2_HUMAN  | WAKLYSLVIWGCTLLLSSPMLVFRTMK <del>E</del> YSD <del>E</del> GHNVTACVISYPSL <del>I</del> WEVFTNM <del>L</del> NNVG                               |
| BRB2_MOUSE  | FLLPLSVITFC <del>T</del> VR <del>I</del> QVLRNNEMKKFKE <del>Q</del> TER <del>I</del> ATVLVLAVLGLFV <del>C</del> W <del>P</del> FQISTFL        |
| BRB2_RAT    | FLLPLS <del>T</del> ITFC <del>T</del> VRIMQVLRNNEMKKFKE <del>Q</del> TER <del>I</del> ATVLVLAVLGLFV <del>C</del> W <del>P</del> FQISTFL       |
| BRB2_RABBIT | FLLPLSVITFC <del>T</del> TVQ <del>I</del> QVLRNNEMQKFKE <del>I</del> QTER <del>T</del> ATVLVLAVLAVLLL <del>F</del> V <del>C</del> WLPFQISTFL  |
| BRB2_CAVPO  | FLLPLS <del>T</del> ITFC <del>T</del> TVQIMQVLRNNEMQKFKE <del>I</del> QTER <del>T</del> ATVLVLAVLAVLLL <del>F</del> V <del>C</del> WLPFQIGTFL |
| BRB2_HUMAN  | FLLPLSVITFC <del>T</del> QIMQVLRNNEMQKFKE <del>I</del> QTER <del>T</del> ATVLVLAVLLL <del>F</del> V <del>C</del> WLPFQISTFL                   |
| BRB2_MOUSE  | DTLLRLGVLSGCWDEHA <del>D</del> VITQISSYAYSN <del>S</del> LNPLVYVIVGKRFRKSREVYRVI <del>C</del> Q   |
| BRB2_RAT    | DTLLRLGVLSGCWNERA <del>D</del> VITQISSYAYSN <del>S</del> CLNPLVYVIVGKRFRKSREVYQA <del>A</del> CP  |
| BRB2_RABBIT | DTLL <del>K</del> LGVLSSCWDEHA <del>D</del> VITQISSYAYSN <del>S</del> CLNPLVYVIVGKRFRKSREVYRAACP  |
| BRB2_CAVPO  | DTLRLLGFLPGCW.EH <del>M</del> DITQISSYAYSN <del>S</del> CLNPLVYVIVGKRFRKSREVYHGLCR  |
| BRB2_HUMAN  | DTLHLRLG <del>L</del> SSC <del>D</del> ER <del>E</del> IVDITQIAS <del>Y</del> AYSN <del>S</del> CLNPLVYVIVGKRFRKSWEVYQCN <del>C</del> Q       |
| *           |   |
| BRB2_MOUSE  | K <del>G</del> CMGEPVQ <del>M</del> ENSMG <del>T</del> LRTSISVERQ <del>I</del> HKLQDWAGK <del>R</del> Q~~~~~                                  |
| BRB2_RAT    | K <del>G</del> GMGE <del>S</del> VQ <del>M</del> ENSMG <del>T</del> LRTSISVERQ <del>I</del> HKLQDWAGM <del>N</del> Q~~~~~                     |
| BRB2_RABBIT | K <del>G</del> CVLEPVQA <del>E</del> SSM <del>G</del> T <del>L</del> R <del>T</del> SISVERQ <del>I</del> HKLPEWTRSSQ~~~~~                     |
| BRB2_CAVPO  | S <del>G</del> CVSEPAQ <del>S</del> ENSMG <del>T</del> LRTSISVERQ <del>I</del> HKLQDWARS <del>S</del> SEGTP <del>P</del> GLL                  |
| BRB2_HUMAN  | K <del>G</del> CRSEPIQ <del>M</del> ENSMG <del>T</del> LRTSISVERQ <del>I</del> HKLQDWAGS <del>R</del> Q~~~~~                                  |

Figure 21A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCGTCC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCCGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCCGA **GNCAGGCCG** GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTTTG AGCATCCCCA CATTCCGTCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATC**N**TGC TCCTCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I **X** L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGG**A**GGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGC**NG** GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V **X** G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 21B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGAT GGGC**CNGCTC** 960  
299 F F A F T N S S L N P V I Y V F V G **X** L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 22A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
 61 CAGTTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120  
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
 1 M D N V L P V D S D 10  
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCTGTGCA ACCAGCCTGG 300  
 11 L S P N I S T N T S E P N Q F V Q P A W 30  
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
 31 Q I V L W A A A Y T V I V V T S V V G N 50  
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420  
 51 V V V M W I I L A H K R M R T V T N Y F 70  
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
 71 L V N L A F A E A S M A A F N T V V N F 90  
 481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTTC 540  
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
 541 TT~~N~~CCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
 111 F P I A A V F A S I Y S M T A V A F D R 130  
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCA CCACAGCCAC CAAAGTGGTC 660  
 131 Y M A I I H P L Q P R L S A T A T K V V 150  
 661 ATCTGTGTCA T~~N~~TGGGTCTT GGCTCTCCTG CTGGCCTTC CCCAGGGCTA CTACTCAACC 720  
 151 I C V I W V L A L L L A F P Q G Y Y S T 170  
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
 171 T E T M P S R V V C M I E W P E H P N K 190  
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840  
 191 I Y E K V Y H I C V T V L I Y F L P L L 210  
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
 211 V I G Y A Y T V V G I T L W A S E I P G 230  
 901 GACTCCTCTG ACCGCTACCA CGAGCAAAGTC TCTGCCAACG GCAAGGTGGT CAAAATGATG 960  
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCCATCA TCTACTGCTG CCTCAATGAC 1140  
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACCGAGGA GGAGCCAGAG 1320  
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAAATGCTC TTCACGAAGT 1380  
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
 391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCTTTGG CAGGTGCAGC CCCCAC TGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTGGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCAATGCGAG TGCTCATTTTC AGGATG 1766

D0053 NP

Figure 23A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60  
61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
1 M A S R L T L L T L L L L L A G D R A 20  
121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
21 S S N P N A T S S S S Q D P E S L Q D R 40  
181 GGCGAAGGGA AGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCCTG 240  
41 G E G K V A T T V I S K M L F X E P I L 60  
241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
61 E V S S L P T T N S T T N S A T K I T A 80  
301 AATACCAACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
81 N T T D E P T T Q P T T E P T T Q P T I 100  
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
121 S F C P G P V T L C S D L E S H S T E A 140  
481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCTT CTCAGNAATG 540  
141 V L G D A L V D F S L K L Y H A F S X M 160  
541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
161 K K V E T N M A F S P F S I A S L L T Q 180  
601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
181 V L L G A G Q N T K T N L E S I L S Y P 200  
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
201 K D F T C V H Q A L K G F T T K G V T S 220  
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTGT GAATGCCTCT 780  
221 V S Q I F H S P D L A I R D T F V N A S 240  
781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
241 R T L Y S S S P R V L S N N S D A N L E 260  
841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
261 L I N T W V A K N T N N K I S R L L D S 280  
901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960  
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 23B

961 ACAACATTTG ATCCCAAGAA AACCAAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGAA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAAATGGA ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCGGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAC 1826

Figure 24

1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCAC ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T X E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACCAAGAGAA TTTCTCATTT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C X K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 25A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCCGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGGGG GGGCCTTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCCTA GGATTGTGGA GTTAAATATT CTGGGTTTC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGCCCC TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

**Figure 25B**

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 26A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTACACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTC AACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

**Figure 26B**

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTG ATGTCTTG GT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTTCTGGC GGAATTAAGA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 27A

1 CTGTGCATGG CATCATCCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I V L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 27B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

D0053 NP

Figure 28A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCAAC 240  
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACACCTGC 480  
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTC TCCTACCACT GGCTGCGATC 660  
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
219 V F F N Y H I L A S L R T R K E V S R T 238

721 AGAGTGCAGGG GGCGAACAGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCTGGTCT GCTGGCCCC TTACCACTTC TTTGCCTTC TGGAATTCTT ATTCCAGGTG 840  
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCAAC 900  
279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 28B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 29A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTT GTGAGGACTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG AACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCG GATGCGCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCA 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCA 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 29B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC T TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

Figure 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCACT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTG GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTG ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 29D**

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

Figure 30A

1 ATGTTCTCTC CCTGGAAGAT ATCAAATGTT CTGTCTGTC GTGAGGACTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCG GATGCGCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCAATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCAATC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 30B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCATTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT ACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

**Figure 30C**

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTG GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 30D**

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

Figure 31A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTT CTGTCTGTC GTGAGGACTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTGCGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCG GATGCGCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCAATC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K E G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT ACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACATCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

**Figure 31C**

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCACT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 31D**

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

**Figure 32A**

|     |   |     |
|-----|---|-----|
| 1   | CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTAGTCTA      | 60  |
| 61  | GGGAAAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGTGTCAGCTCTCCTG       | 120 |
| 1   | M S S S S W   | 6   |
| 121 | GCTCCTCTCAGCCTGTTGCTGTAAGTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA      | 180 |
| 7   | L L L S L V A V T A A Q S T I E E Q A K                         | 26  |
| 181 | GACATTTGGACAAGTTAACACCAATATTACTGAAGAGAAATGTCCAAACATGAATAATGCTGC | 240 |
| 27  | T F L D K F N H E A E D L F Y Q S S L A                         | 46  |
| 241 | TTCTTGGAAATTATAACACCAATATTACTGAAGAGAAATGTCCAAACATGAATAATGCTGG   | 300 |
| 47  | S W N Y N T N I T E E N V Q N M N N A G                         | 66  |
| 301 | GGACAAATGGTCTGCCTTTAAAGGAACAGTCCACACTTGCCCAATGTATCCACTACA       | 360 |
| 67  | D K W S A F L K E Q S T L A Q M Y P L Q                         | 86  |
| 361 | AGAAATTCAAGAACAGCTCACAGTCAAGCTTCAGCTGCAGGCTCTCAGCAAAATGGTCTTC   | 420 |
| 87  | E I Q N L T V K L Q L Q A L Q Q N G S S                         | 106 |
| 421 | AGTGCTCTCAGAACAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAC       | 480 |
| 107 | V L S E D K S K R L N T I L N T M S T I                         | 126 |
| 481 | CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAAATGCTTATTACTGAACC     | 540 |
| 127 | Y S T G K V C N P D N P Q E C L L L E P                         | 146 |
| 541 | AGTTTGAATGAAATAATGGCAAACAGTTAGACTACAATGAGAGGCTCTGGCTTGGGA       | 600 |
| 147 | G L N E I M A N S L D Y N E R L W A W E                         | 166 |
| 601 | AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGCTT     | 660 |
| 167 | S W R S E V G K Q L R P L Y E E Y V V L                         | 186 |
| 661 | GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGATTATTGGAGAGGAGA     | 720 |
| 187 | K N E M A R A N H Y E D Y G D Y W R G D                         | 206 |
| 721 | CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGGCCAGTTGATTGAAGATGT       | 780 |
| 207 | Y E V N G V D G Y D Y S R G Q L I E D V                         | 226 |
| 781 | GGAACATACCTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC     | 840 |
| 227 | E H T F E E I K P L Y E H L H A Y V R A                         | 246 |
| 841 | AAAGTTGATGAATGCCTATCCTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATT      | 900 |
| 247 | K L M N A Y P S Y I S P I G C L P A H L                         | 266 |

**Figure 32B**

|      |   |             |
|------|---|-------------|
| 901  | GCTTGGTGATATGTGGGGTAGATTTGGACAAATCTGTA<br>267    L G D M W G R F W T N L Y S L T V P F G        | 960<br>286  |
| 961  | ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGC<br>287    Q K P N I D V T D A M V D Q A W D A Q R | 1020<br>306 |
| 1021 | AATATTCAAGGAGGCCGAGAAGTTCTTGATCTGTTGGCTTC<br>307    I F K E A E K F F V S V G L P N M T Q G     | 1080<br>326 |
| 1081 | ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTT<br>327    F W E N S M L T D P G N V Q K A V C H P      | 1140<br>346 |
| 1141 | CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATC<br>347    T A W D L G K G D F R I L M C T K V T M          | 1200<br>366 |
| 1201 | GGACGACTTCCTGACAGCTCATGAGATGGGG<br>367    D D F L T A H H E M G H I Q Y D M A Y A               | 1260<br>386 |
| 1261 | TGCACAACCTTTCTGCTAACGAAATGGAGCT<br>387    A Q P F L L R N G A N E G F H E A V G E               | 1320<br>406 |
| 1321 | AATCATGTCACTTCTGCAGCCACAC<br>407    I M S L S A A T P K H L K S I G L L S P                     | 1380<br>426 |
| 1381 | CGATTTCAAGAAGACAATGAAACAGAAATA<br>427    D F Q E D N E T E I N F L L K Q A L T I                | 1440<br>446 |
| 1441 | TGTTGGGACTCTGCCATTACTACATGTTAGAGAAGTGGAGGTGG<br>447    V G T L P F T Y M L E K W R W M V F K G  | 1500<br>466 |
| 1501 | GGAAATTCCAAAGACCAGTGGATGAAAAAGTGGTGGAGATGA<br>467    E I P K D Q W M K K W W E M K R E I V G    | 1560<br>486 |
| 1561 | GGTGGTGGAACCTGTGCCCATGATGAAACATA<br>487    V V E P V P H D E T Y C D P A S L F H V              | 1620<br>506 |
| 1621 | TTCTAATGATTACTCATTGATATTACACAAGGACC<br>507    S N D Y S F I R Y Y T R T L Y Q F Q F Q           | 1680<br>526 |
| 1681 | AGAAGCACTTGTCAAGCAGCTAACATGAAGGCC<br>527    E A L C Q A A K H E G P L H K C D I S N             | 1740<br>546 |

**Figure 32C**

|      |   |      |
|------|---|------|
| 1741 | CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCCTG | 1800 |
| 547  | S T E A G Q K L F N M L R L G K S E P W                       | 566  |
| 1801 | GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA  | 1860 |
| 567  | T L A L E N V V G A K N M N V R P L L N                       | 586  |
| 1861 | CTACTTTGAGGCCCTTACCTGGCTGAAAGACCAGAACAGAACAGAATTCTTTGTGGGATG  | 1920 |
| 587  | Y F E P L F T W L K D Q N K N S F V G W                       | 606  |
| 1921 | GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC  | 1980 |
| 607  | S T D W S P Y A D Q S I K V R I S L K S                       | 626  |
| 1981 | AGCTCTGGAGATAAACGATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC   | 2040 |
| 627  | A L G D K A Y E W N D N E M Y L F R S S                       | 646  |
| 2041 | TGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAATCAGATGATTCTTTGG       | 2100 |
| 647  | V A Y A M R Q Y F L K V K N Q M I L F G                       | 666  |
| 2101 | GGAGGAGGATGTGCGAGTGGCTAATTGAAACCAAGAACCTCCTTAATTCTTGTAC       | 2160 |
| 667  | E E D V R V A N L K P R I S F N F F V T                       | 686  |
| 2161 | TGCACCTAAAAATGTGTCTGATATCATTCTAGAACTGAAGTTGAAAAGGCCATCAGGAT   | 2220 |
| 687  | A P K N V S D I I P R T E V E K A I R M                       | 706  |
| 2221 | GTCCCGGAGCCGTATCAATGATGCTTCCGTCTGAATGACAACAGCCTAGAGTTCTGG     | 2280 |
| 707  | S R S R I N D A F R L N D N S L E F L G                       | 726  |
| 2281 | GATACAGCCAACACTGGACCTCCTAACCAAGCCCCCTGTTCCATATGGCTGATTGTTT    | 2340 |
| 727  | I Q P T L G P P N Q P P V S I W L I V F                       | 746  |
| 2341 | TGGAGTTGTATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG   | 2400 |
| 747  | G V V M G V I V V G I V I L I F T G I R                       | 766  |
| 2401 | AGATCGGAAGAAGAAAAATAAGCAAGAACAGTGGAGAAAATCCTTATGCCTCCATCGATAT | 2460 |
| 767  | D R K K N K A R S G E N P Y A S I D I                         | 786  |
| 2461 | TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTCAGACCTCCTTTA    | 2520 |
| 787  | S K G E N N P G F Q N T D D V Q T S F *                       | 806  |
| 2521 | GAAAAATCTATGTTTCTCTTGAGGTGATTTGTATGTAATGTTAATTTCATGG          | 2580 |
| 2581 | TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA   | 2640 |

**Figure 32D**

|      |  |      |
|------|--|------|
| 2641 | AAAAAAATTGTCAAAGACAACATGCCAAGGAGAGGCATCTCATTGACATTGCTTC      | 2700 |
| 2701 | AGTATTATTTCTGTCTGGATTGACTCTGTTCTGTTCTTAATAAGGATTTGTAT        | 2760 |
| 2761 | TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAAGGATAATCTAAAT | 2820 |
| 2821 | GTAATGTCTGTTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG    | 2880 |
| 2881 | GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGAACTGGTAGC    | 2940 |
| 2941 | TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCATTAAATCCATTGTCAAGGATGA  | 3000 |
| 3001 | CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTATTTGCCTACAGTGATGTTT    | 3060 |
| 3061 | GGAATCGATCATGCTTCTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGAAACAG   | 3120 |
| 3121 | GTAGAGGACATTGCTTTCACTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA    | 3180 |
| 3181 | AACTAGAGCCAGGGGCCTCGTGAACCTCCCAGAGCATGCCTGATAGAAACTCATTCTAC  | 3240 |
| 3241 | TGTTCTCAACTGTGGAGTGAATGGAAATTCCAACGTATGTTCACCCCTCTGAAGTGGGT  | 3300 |
| 3301 | ACCCAGTCTCTAAATCTTGCTCACAGTGTGAGCAGTGCTGAGCACAAAG            | 3360 |
| 3361 | CAGACACTCAATAATGCTAGATTACACACTCAAAAAAAAAAA                   | 3405 |

**Figure 33A**

|     |   |     |
|-----|---|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC     | 60  |
| 1   | M H L I D Y L L L L V G L L A L S H G                         | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                       | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAAGCCCCTGCCAATGCTGACTTTGCCTTC | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                       | 60  |
| 181 | CGCTTCTACTACCTGATCGCTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG       | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                       | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCAGCCAG       | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                       | 100 |
| 301 | ATCCTTGAGGGCCTGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC    | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                       | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACCGCGTGGC  | 420 |
| 121 | F Q H L L H T L N L P G H G L E T R V G                       | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCTTGCAAAATTCTGAATGACACCAG      | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                       | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGCACAATCCAG    | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                       | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG   | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                       | 200 |
| 601 | CTCAAGAAGGACGTCTGATGGTGCCTGGTAATTACATTACTCAAAGCCCTGTGGAG      | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                       | 220 |
| 661 | AAACCATTCAATTCCCTCAAGGACCACCTCCAAAGACTCTATGTTGATGAGAACACAACA  | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                       | 240 |
| 721 | GTCCGGGTGCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATA     | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                       | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC     | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                       | 280 |

**Figure 33B**

|      |  |      |
|------|--|------|
| 841  | CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                      | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAAGCTAGAGTTGCATCTCCCAAG     | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                      | 320  |
| 961  | TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT     | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                      | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAAACAGCAAAACTGGAGGCATCC  | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                      | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                      | 380  |
| 1141 | ACCACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC      | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                      | 400  |
| 1201 | CGGCCCTTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCTCTGGCAAG         | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                      | 420  |
| 1261 | GTCGTCGACCCCACGAAACCATAG                                     | 1284 |
| 421  | V V D P T K P *  | 428  |

**Figure 34A**

|     |  |     |
|-----|--|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC    | 60  |
| 1   | M H L I D Y L L L L V G L L A L S H G                        | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                      | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC  | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                      | 60  |
| 181 | CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG     | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                      | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG    | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                      | 100 |
| 301 | ATCCTTGAGGGCCTGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC   | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                      | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACCGCGTGGC | 420 |
| 121 | F Q H L L H T L N L P G H G L E T R V G                      | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCTTGCAAAATTCTGAATGACACCATG    | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                      | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                      | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG  | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                      | 200 |
| 601 | CTCAAGAAGGACGTCTTGATGGTGCCTGAATTACATTACTCAAAGCCCTGTGGAG      | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                      | 220 |
| 661 | AAACCATTCAATTCTCAAGGACCCTCCAAAGACTTTATGTTGATGAGAACACAACA     | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                      | 240 |
| 721 | GTCCGGGTGCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATA    | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                      | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC    | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                      | 280 |

**Figure 34B**

|      |  |      |
|------|--|------|
| 841  | CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                      | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAACGCTAGAGTTGCATCTTCCCAAG   | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                      | 320  |
| 961  | TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT     | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                      | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAAACAGCAAAAATGGAGGCATCC  | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                      | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                      | 380  |
| 1141 | ACCACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCAGATTCAAC     | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                      | 400  |
| 1201 | CGGCCCTCCTTGTTGATCTTCCACCAGCACCCAGAGTGTCTCTGGCAAG            | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                      | 420  |
| 1261 | GTCGTCGACCCCACGAAACCATAG 1284                                |      |
| 421  | V V D P T K P * 428  |      |

**Figure 35A**

|     |  |     |
|-----|--|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC    | 60  |
| 1   | M H L I D Y L L L L V G L L A L S H G                        | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                      | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                      | 60  |
| 181 | CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG     | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                      | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG    | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                      | 100 |
| 301 | ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC  | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                      | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACCGCGTGGC | 420 |
| 121 | F Q H L L H T L N L P G H G L E T R V G                      | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCAG    | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                      | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGCACAATCCAG   | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                      | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGCGAG | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                      | 200 |
| 601 | CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTACTTCAAAGCCCTGTGGAG   | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                      | 220 |
| 661 | AAACCATTCAATTCCCTCAAGGACCCTCCAAAGACTTCTATGTTGATGAGAACACAACA  | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                      | 240 |
| 721 | GTCCGGGTGCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATA    | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                      | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC    | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                      | 280 |

**Figure 35B**

|      |  |      |
|------|--|------|
| 841  | CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                      | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAAGCTAGAGTTGCATCTCCCAAG     | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                      | 320  |
| 961  | TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT     | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                      | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC   | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                      | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                      | 380  |
| 1141 | ACCACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC      | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                      | 400  |
| 1201 | CGGCCCTTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGGCAAG    | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                      | 420  |
| 1261 | GTCGTCGACCCCCACGAAACCATAG                                    | 1284 |
| 421  | V V D P T K P *  | 428  |

**Figure 36A**

|     |   |     |
|-----|---|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGCCCTTCATGGC      | 60  |
| 1   | M H L I D Y L L L V G L L A L S H G                           | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCACCAGCAGATTCTG   | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                       | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAAGCCCCTGCCAATGCTGACTTTGCCTTC | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                       | 60  |
| 181 | CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG      | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                       | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCTGCTCACACAGCCAGCCAG        | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                       | 100 |
| 301 | ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC   | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                       | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACCGCGTGGC  | 420 |
| 121 | F Q H L L H T L N L P G H G L E T R V G                       | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCTGAATGACACCAG     | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                       | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGCACAATCCAG    | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                       | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGNGAG   | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                       | 200 |
| 601 | CTCAAGAAGGACGTCTGATGGTGCCTGAATTACATTACTCAAAGCCCTGTGGAG        | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                       | 220 |
| 661 | AAACCATTCAATTCTCAAGGACCACTCCAAAGACTNTATGTTGATGAGAACACAACA     | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                       | 240 |
| 721 | GTCCGGGTGCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATA    | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                       | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC     | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                       | 280 |

**Figure 36B**

|      |   |      |
|------|---|------|
| 841  | CCTAACCAAGGCAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                     | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTCACAAGAAGCTAGAGTTGCATCTCCCAAG   | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                     | 320  |
| 961  | TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTGCCCCAGGCTGGGCTCACGGAT   | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                     | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC  | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                     | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC  | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                     | 380  |
| 1141 | ACCACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC     | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                     | 400  |
| 1201 | CGGCCCTCCTTGTTGATCTTCCACCAGCACCCAGAGTGTCTCTGGCAAG           | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                     | 420  |
| 1261 | GTCGTCGACCCCCACGAAACCATAG                                   | 1284 |
| 421  | V V D P T K P *   | 428  |

**Figure 37A**

|     |  |     |
|-----|--|-----|
| 1   | CGCCCAACCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTAGTCTA    | 60  |
| 61  | GGGAAAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTCCTG  | 120 |
| 1   | M S S S S W  | 6   |
| 121 | GCTCCTTCTCAGCCTTGTGCTGTAAGTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA  | 180 |
| 7   | L L L S L V A V T A A Q S T I E E Q A K                      | 26  |
| 181 | GACATTTTGACAAGTTAACACCGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC    | 240 |
| 27  | T F L D K F N H E A E D L F Y Q S S L A                      | 46  |
| 241 | TTCTTCCAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG | 300 |
| 47  | S W N Y N T N I T E E N V Q N M N N A G                      | 66  |
| 301 | GGACAAATGGTCTGCCTTTAAAGGAACAGTCCACACTTGCCAAATGTATCCACTACA    | 360 |
| 67  | D K W S A F L K E Q S T L A Q M Y P L Q                      | 86  |
| 361 | AGAAATTCAAGATCTCACAGTCAGCTTCAGCTGCAGGCTTTCAGCAAAATGGTCTTC    | 420 |
| 87  | E I Q N L T V K L Q L Q A L Q Q N G S S                      | 106 |
| 421 | AGTGCTCTCAGAAGACAAGAGCAAACGGTTAACACAAATTCTAAATACAATGAGCACCAT | 480 |
| 107 | V L S E D K S K R L N T I L N T M S T I                      | 126 |
| 481 | CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC  | 540 |
| 127 | Y S T G K V C N P D N P Q E C L L L E P                      | 146 |
| 541 | AGGTTGAATGAAATAATGGCAAACAGTTAGACTACAATGAGAGGCTCTGGCTTGGGA    | 600 |
| 147 | G L N E I M A N S L D Y N E R L W A W E                      | 166 |
| 601 | AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT | 660 |
| 167 | S W R S E V G K Q L R P L Y E E Y V V L                      | 186 |
| 661 | GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGATTATTGGAGAGGAGA  | 720 |
| 187 | K N E M A R A N H Y E D Y G D Y W R G D                      | 206 |
| 721 | CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGGCCAGTTGATTGAAGATGT    | 780 |
| 207 | Y E V N G V D G Y D Y S R G Q L I E D V                      | 226 |
| 781 | GGAACATACCTTGAAGAGATTAACCATTATGAACATCTCATGCCTATGTGAGGGC      | 840 |
| 227 | E H T F E E I K P L Y E H L H A Y V R A                      | 246 |
| 841 | AAAGTTGATGAATGCCTATCCTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT  | 900 |
| 247 | K L M N A Y P S Y I S P I G C L P A H L                      | 266 |

**Figure 37B**

|      |  |      |
|------|--|------|
| 901  | GCTTGGTGATATGTGGGGTAGATTGGACAAATCTGACTCTTGACAGTCCCTTGG       | 960  |
| 267  | L G D M W G R F W T N L Y S L T V P F G                      | 286  |
| 961  | ACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGATGCACAGAG   | 1020 |
| 287  | Q K P N I D V T D A M V D Q A W D A Q R                      | 306  |
| 1021 | AATATTCAAGGGAGGCCGAGAAGTTCTTGATCTGTTGGCTTCCTAATATGACTCAAGG   | 1080 |
| 307  | I F K E A E K F F V S V G L P N M T Q G                      | 326  |
| 1081 | ATTCTGGAAAATTCCATGCTAACGGACCCAGGAAATGTTAGAAAGCAGTCTGCCATCC   | 1140 |
| 327  | F W E N S M L T D P G N V Q K A V C H P                      | 346  |
| 1141 | CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT  | 1200 |
| 347  | T A W D L G K G D F R I L M C T K V T M                      | 366  |
| 1201 | GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC | 1260 |
| 367  | D D F L T A H H E M G H I Q Y D M A Y A                      | 386  |
| 1261 | TGCACAAACCTTTCTGCTAACGAAATGGAGCTAACGATTCCATGAAGCTGTTGGGA     | 1320 |
| 387  | A Q P F L L R N G A N E G F H E A V G E                      | 406  |
| 1321 | AATCATGTCACTTCTGCAGCCACACCTAACGATTTAAATCCATTGGTCTTGTCAACC    | 1380 |
| 407  | I M S L S A A T P K H L K S I G L L S P                      | 426  |
| 1381 | CGATTTCAAGAAGACAATGAAACAGAAATAAACCTCCTGCTCAAACAAGCACTCACGAT  | 1440 |
| 427  | D F Q E D N E T E I N F L L K Q A L T I                      | 446  |
| 1441 | TGTTGGGACTCTGCCATTTACTACATGTTAGAGAAGTGGAGGTGGATGGTCTTAAAGG   | 1500 |
| 447  | V G T L P F T Y M L E K W R W M V F K G                      | 466  |
| 1501 | GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGAGATGAAGCGAGAGATAGTTGG  | 1560 |
| 467  | E I P K D Q W M K K W W E M K R E I V G                      | 486  |
| 1561 | GGTGGTGGAACCTGTGCCCATGATGAAACATACTGTGACCCCGCATCTGTTCCATGT    | 1620 |
| 487  | V V E P V P H D E T Y C D P A S L F H V                      | 506  |
| 1621 | TTCTAACATGATTACTCATTGATATTACACAGGACCCCTTACCAATTCCAGTTCA      | 1680 |
| 507  | S N D Y S F I R Y Y T R T L Y Q F Q F Q                      | 526  |
| 1681 | AGAACGACTTTGTCAAGCAGCTAACATGAAGGCCCTTGCACAAATGTGACATCTCAA    | 1740 |
| 527  | E A L C Q A A K H E G P L H K C D I S N                      | 546  |

**Figure 37C**

|      |   |      |
|------|---|------|
| 1741 | CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCCTG | 1800 |
| 547  | S T E A G Q K L F N M L R L G K S E P W                       | 566  |
| 1801 | GACCCTAGCATTGGAAAATGTTGAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA   | 1860 |
| 567  | T L A L E N V V G A K N M N V R P L L N                       | 586  |
| 1861 | CTACTTTGAGCCCTTATTCACCTGGCTGAAAGACCAGAACACAAGAATTCTTTGTGGATG  | 1920 |
| 587  | Y F E P L F T W L K D Q N K N S F V G W                       | 606  |
| 1921 | GAGTACCGACTGGAGTCCATATGCAGACCAAGCATCAAAGTGAGGATAAGCCTAAAATC   | 1980 |
| 607  | S T D W S P Y A D Q S I K V R I S L K S                       | 626  |
| 1981 | AGCTCTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC   | 2040 |
| 627  | A L G D K A Y E W N D N E M Y L F R S S                       | 646  |
| 2041 | TGTTGCATATGCTATGAGGCAGTACTTTTAAAAGTAAAAATCAGATGATTCTTTGG      | 2100 |
| 647  | V A Y A M R Q Y F L K V K N Q M I L F G                       | 666  |
| 2101 | GGAGGAGGATGTGCGAGTGGCTAATTGAAACCAAGAACATCCTTAATTCTTGTAC       | 2160 |
| 667  | E E D V R V A N L K P R I S F N F F V T                       | 686  |
| 2161 | TGCACCTAAAAACGTGTCTGATATCATTCTAGAACTGAAGTTGAAAAGGCCATCAGGAT   | 2220 |
| 687  | A P K N V S D I I P R T E V E K A I R M                       | 706  |
| 2221 | GTCCCGGAGCCGTATCAATGATGCTTCCGCTCTGAATGACAACAGCCTAGAGTTCTGG    | 2280 |
| 707  | S R S R I N D A F R L N D N S L E F L G                       | 726  |
| 2281 | GATACAGCCAACACTTGGACCTCTAACCAAGCCCCCTGTTCCATATGGCTGATTGTTT    | 2340 |
| 727  | I Q P T L G P P N Q P P V S I W L I V F                       | 746  |
| 2341 | TGGAGTTGTATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG   | 2400 |
| 747  | G V V M G V I V V G I V I L I F T G I R                       | 766  |
| 2401 | AGATCGGAAGAAGAAAAATAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT   | 2460 |
| 767  | D R K K K N K A R S G E N P Y A S I D I                       | 786  |
| 2461 | TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTAGACCTCCTTTA    | 2520 |
| 787  | S K G E N N P G F Q N T D D V Q T S F *                       | 806  |
| 2521 | GAAAAATCTATGTTTCTCTTGAGGTGATTTGTTATGTAATGTTAATTTCATGG         | 2580 |
| 2581 | TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA   | 2640 |

**Figure 37D**

|      |  |      |
|------|--|------|
| 2641 | AAAAAAATTGTCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC  | 2700 |
| 2701 | AGTATTATTTCTGTCTCTGGATTGACTCTGTTCTGTTCTTAATAAGGATTTGTAT      | 2760 |
| 2761 | TAGAGTATATTAGGAAAGTGTATTTGGTCTCACAGGCTGTTCAAGGATAATCTAAAT    | 2820 |
| 2821 | GTAAATGTCTGTTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG   | 2880 |
| 2881 | GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGAACTGGTAGC    | 2940 |
| 2941 | TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCATTAATCCATTGTCAAGGATGA   | 3000 |
| 3001 | CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCAACAGTGATGTT    | 3060 |
| 3061 | GGAATCGATCATGCTTCTCAAGGTGACAGGTCTAAAGAGAGAAGAACAG            | 3120 |
| 3121 | GTAGAGGACATTGCTTTCACTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA    | 3180 |
| 3181 | AACTAGAGCCAGGGGCCTCGTGAACCTCCCAGAGCATGCCTGATAGAAACTCATTCTAC  | 3240 |
| 3241 | TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACGTATGTTCACCCCTCTGAAGTGGGT | 3300 |
| 3301 | ACCCAGTCTCTAAATCTTGCTACAGTGTGAGCAGTGCTGAGCACAAAG             | 3360 |
| 3361 | CAGACACTCAATAATGCTAGATTACACACTCAAAAAAAAAAA                   | 3405 |

Figure 38A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTN CTGAGGNCTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V X E X S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTTCTGGG CCATCACCAT CTCACAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTTGGGA GACCCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCG GATGCGCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 38B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATH GANGTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K X G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCTCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

**Figure 38C**

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAGT GTCTGGCACCA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAACGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 38D**

3241 ATTCCCTCCT TACCCCCAAC CCACTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCGAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAA AAA 3733

D0053 NP

A

A

G C A

A/G

SNP1 (A/G)

G

G C

G/C

SNP2 (G/C)

C

A G C

C/A

SNP3 (C/A)

B

A

G G A

C C

C

G C C

A G A

D

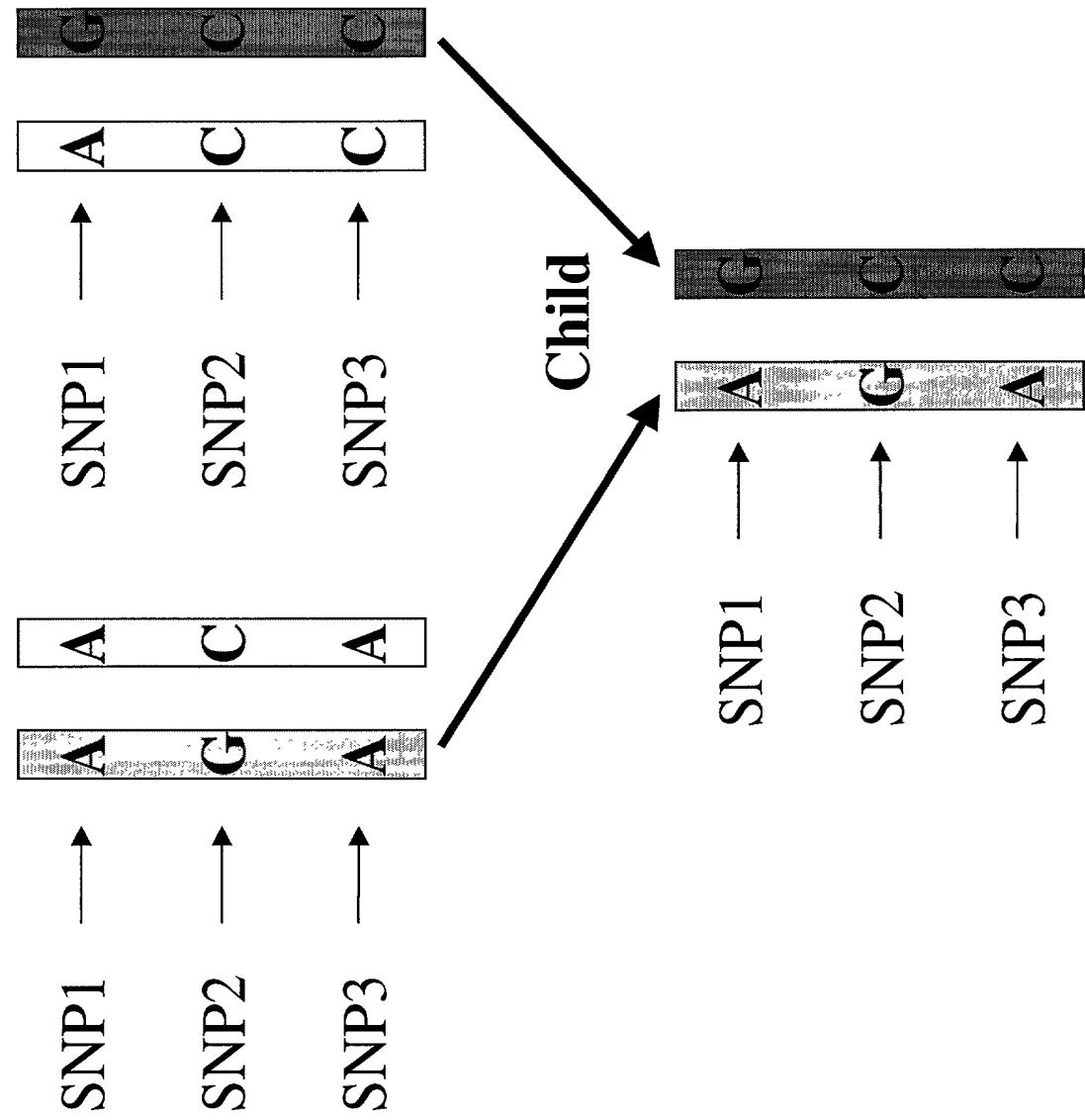
G G C

A C A

Figure 39

Figure 40

Father      Mother



D0053 NP

Figure 41A

1 CACCCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
181 AGGCCTGAAG GAACAGGCCG GGGAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240  
241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CCGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
1 M A R A H W G C C P W L 12  
301 GTCCCTCCTCT GTGCTTGTGC CTGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
13 V L L C A C A W G H T K P L D L G G Q D 32  
361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
33 V R N C S T N P P Y L P V T V V N T T M 52  
421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
481 GGCACAGATG CTCACATGAA CGACTACATC GGCAACATG ACGAGAGGCG TGGTGGATT 540  
73 G T D A H M N E Y I G Q H D E R R A W I 92  
541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600  
93 T G F T G S A G T A V V T M K K A A V W 112  
601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
113 T D S R Y W T Q A E R Q M D C N W E L H 132  
661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720  
133 K E V G T T P I V T W L L T E I P A G G 152  
721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
153 R V G F D P F L L S I D T W E S Y D L A 172  
781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840  
173 L Q G S N R Q L V S I T T N L V D L V W 192  
841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900  
193 G S E R P P V P N Q P I Y A L Q E A F T 212  
901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAG 960  
213 G S T W Q E K V S G V R S Q M Q K H Q K 232

D0053 NP

Figure 41B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080  
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGTA CTTGGCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440  
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAATG CTGCCCTGGC CCACTACAGC 1560  
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTCCCCG CTGCTACATC AGGGCGAACATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800  
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGACAA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
513 D A G L N Y G H G T G H G I G N F L C V 532

D0053 NP

Figure 41C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980  
553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100  
593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCAGAGTG GCTTCAACAGCACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
673 V \* 673

2341 GCTCCCTCA CCCTGCCTG AACATACCCC AAGAGCCCCCT GCTGGCCCAT TGCCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCATAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACCC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

D0053 NP

Figure 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCCTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

Figure 42A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18  
  
 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38  
  
 121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58  
  
 181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78  
  
 241 CTGGCAGCCT CTGATCTGGT GTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98  
  
 301 AACAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118  
  
 361 GCCAATTGT TCATCAGCAT CTTCCGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138  
  
 421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCCGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158  
  
 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCGTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178  
  
 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198  
  
 601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218  
  
 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238  
  
 721 AGAGTGC~~A~~GG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V Q G P K D S K T T A L I L T L V V A 258  
  
 781 TTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278  
  
 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

**Figure 42B**

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

Figure 43A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTT CTGTCTGTC GTGAGGCCTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E A S V P T 20  
  
 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40  
  
 121 ACCTTGCC AGAGCAAATG CCCCCAAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60  
  
 181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80  
  
 241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100  
  
 301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCTCTGGG CCATCACCAT CTCCAACAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120  
  
 361 TTGACTGGC TCTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140  
  
 421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGACCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160  
  
 481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180  
  
 541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200  
  
 601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220  
  
 661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCAATC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240  
  
 721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260  
  
 781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280  
  
 841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

D0053 NP

Figure 43B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCTAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

D0053 NP

Figure 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTG GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAATG AGAAAAAATTG ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAATCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

**Figure 43D**

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

**Figure 44A**

|     |  |     |
|-----|--|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC      | 60  |
| 1   | M H L I D Y L L L L V G L L A L S H G                          | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG   | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                        | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAAGCCCCTGCCAATGCTGACTTTGCCCTTC | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                        | 60  |
| 181 | CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG       | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                        | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG      | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                        | 100 |
| 301 | ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC    | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                        | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACCGCGTGGC   | 420 |
| 121 | F Q H L L H T L N L P G H G L E T R V G                        | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCATG     | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                        | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG    | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                        | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGTGAG   | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                        | 200 |
| 601 | CTCAAGAAGGACGTCTGATGGTGCTGGTGAATTACATTACTCAAAGCCCTGTGGAG       | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                        | 220 |
| 661 | AAACCATTCAATTCCCTCAAGGACCACTCCAAAGACTTCTATGTTGATGAGAACACAACA   | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                        | 240 |
| 721 | GTCCGGGTGCCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATA    | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                        | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC      | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                        | 280 |

**Figure 44B**

|      |  |      |
|------|--|------|
| 841  | CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                      | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAACGCTAGAGTTGCATCTCCCAAG    | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                      | 320  |
| 961  | TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTCACGGAT     | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                      | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC   | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                      | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                      | 380  |
| 1141 | ACGACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCATTCAAC       | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                      | 400  |
| 1201 | CGGCCCTTCCTTGTTGATCTTCCACCAGCACCCAGAGTGTCTCTGGCAAG           | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                      | 420  |
| 1261 | GTCGTCGACCCCCACGAAACCATAG 1284                               |      |
| 421  | V V D P T K P * 428  |      |

**Figure 45A**

|     |  |     |
|-----|--|-----|
| 1   | ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC            | 60  |
| 1   | M H L I D Y L L L L V G L L A L S H G                                | 20  |
| 61  | CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG         | 120 |
| 21  | Q L H V E H D G E S C S N S S H Q Q I L                              | 40  |
| 121 | GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAAGCCCCTGCCAATGCTGACTTTGCCTTC        | 180 |
| 41  | E T G E G S P S L K I A P A N A D F A F                              | 60  |
| 181 | CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG             | 240 |
| 61  | R F Y Y L I A S E T P G K N I F F S P L                              | 80  |
| 241 | AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG            | 300 |
| 81  | S I S A A Y A M L S L G A C S H S R S Q                              | 100 |
| 301 | ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC          | 360 |
| 101 | I L E G L G F N L T E L S E S D V H R G                              | 120 |
| 361 | TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACAT <u>T</u> CGTGGC | 420 |
| 121 | F Q H L L H T L N L P G H G L E T <u>C</u> V G                       | 140 |
| 421 | AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCAG            | 480 |
| 141 | S A L F L S H N L K F L A K F L N D T M                              | 160 |
| 481 | GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG          | 540 |
| 161 | A V Y E A K L F H T N F Y D T V G T I Q                              | 180 |
| 541 | CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG          | 600 |
| 181 | L I N D H V K K E T R G K I V D L V S E                              | 200 |
| 601 | CTCAAGAAGGACGTCTGATGGTGCTGGTGAATTACATTACTTCAAAGCCCTGTGGAG            | 660 |
| 201 | L K K D V L M V L V N Y I Y F K A L W E                              | 220 |
| 661 | AAACCATTCAATTCCCTCAAGGACCACCTCCAAAGACTTCTATGTTGATGAGAACACAACA        | 720 |
| 221 | K P F I S S R T T P K D F Y V D E N T T                              | 240 |
| 721 | GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATA           | 780 |
| 241 | V R V P M M L Q D Q E H H W Y L H D R Y                              | 260 |
| 781 | TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC            | 840 |
| 261 | L P C S V L R M D Y K G D A T V F F I L                              | 280 |

**Figure 45B**

|      |  |      |
|------|--|------|
| 841  | CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG | 900  |
| 281  | P N Q G K M R E I E E V L T P E M L M R                      | 300  |
| 901  | TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAAGCTAGAGTTGCATCTTCCCAAG    | 960  |
| 301  | W N N L L R K R N F Y K K L E L H L P K                      | 320  |
| 961  | TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT     | 1020 |
| 321  | F S I S G S Y V L D Q I L P R L G F T D                      | 340  |
| 1021 | CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAAATGGAGGCATCC   | 1080 |
| 341  | L F S K W A D L S G I T K Q Q K L E A S                      | 360  |
| 1081 | AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   | 1140 |
| 361  | K S F H K A T L D V D E A G T E A A A A                      | 380  |
| 1141 | ACACGTTCGCGATCAAATTCTCTGCCAGACCAATGCCACATCCTGCATTCAAC        | 1200 |
| 381  | T T F A I K F F S A Q T N R H I L R F N                      | 400  |
| 1201 | CGGCCCTCCTTGTTGATCTTCCACCAGCACCCAGAGTGTCTCTGGCAAG            | 1260 |
| 401  | R P F L V V I F S T S T Q S V L F L G K                      | 420  |
| 1261 | GTCGTCGACCCCACGAAACCATAG 1284                                |      |
| 421  | V V D P T K P * 428  |      |

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Figure 46A

1 CACCCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCG CTCCATCCAC 240  
241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
1 M A R A H W G C C P W L 12  
301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
13 V L L C A C A W G H T K P L D L G G Q D 32  
361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
33 V R N C S T N P P Y L P V T V V N T T M 52  
421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540  
73 G T D A H M N E Y I G Q H D E R R A W I 92  
541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTACTA TGAAGAAAGC AGCTGTCTGG 600  
93 T G F T G S A G T A V V T M K K A A V W 112  
601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
113 T D S R Y W T Q A E R Q M D C N W E L H 132  
661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720  
133 K E V G T T P I V T W L L T E I P A G G 152  
721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
153 R V G F D P F L L S I D T W E S Y D L A 172  
781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840  
173 L Q G S N R Q L V S I T T N L V D L V W 192  
841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCAACA 900  
193 G S E R P P V P N Q P I Y A L Q E A F T 212  
901 GGGAGCACTT GGCAGGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 46B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TAFTCCTACA CGCTGCTCAC AGACTCTTCT 1080  
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAAATC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440  
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560  
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTCCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCCGAG AGCCTTGTGG 1800  
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCC~~N~~GAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCCT TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \* 673

2341 GCTCCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCCT GCTGGCCCAT TGCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACCC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

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**Figure 46D**

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428